

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 03/27/2003

PATENT APPLICATION: US/09/857,902

TIME: 12:17:44

Input Set : A:\PTO.txt

Output Set: N:\CRF4\03272003\I857902.raw

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5 <110> APPLICANT: Sedlacek, et al.
7 <120> TITLE OF INVENTION: Spermatogenesis Protein
9 <130> FILE REFERENCE: 4121-125
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/857,902
C--> 12 <141> CURRENT FILING DATE: 2001-06-08
14 <150> PRIOR APPLICATION NUMBER: DE 198 56 882.7
15 <151> PRIOR FILING DATE: 1998-12-10
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn Ver. 2.1.
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1618
25 <212> TYPE: DNA
26 <213> ORGANISM: Human
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (113)..(1087)
33 <400> SEQUENCE: 1
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38 tgtctccgct cgacagggtg cttgggcaga gcccatcggg taggcgcggg cc atg      115
39                                     Met
40                                     1
42 gcg cag tac aag ggc acc atg cgc gag gca ggc cgt gcc atg cac ctc      163
43 Ala Gln Tyr Lys Gly Thr Met Arg Glu Ala Gly Arg Ala Met His Leu
44             5             10             15
46 ctc aag aag cgc gaa agg cag cgg gag cag atg gag gtg ctg aag cag      211
47 Leu Lys Lys Arg Glu Arg Gln Arg Glu Gln Met Glu Val Leu Lys Gln
48             20             25             30
50 cgc atc gcc gag gag acc atc ctc aag tcg cag gtg gac aag agg ttc      259
51 Arg Ile Ala Glu Glu Thr Ile Leu Lys Ser Gln Val Asp Lys Arg Phe
52             35             40             45
54 tcg gcg cat tac gac gcc gtg gag gcc gag ctg aag tcc agc acg gtg      307
55 Ser Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Thr Val
56 50             55             60             65
58 ggc ctg gtg acc ctg aac gac atg aag gcc cgg cag gag gcc ctg gtc      355
59 Gly Leu Val Thr Leu Asn Asp Met Lys Ala Arg Gln Glu Ala Leu Val
60             70             75             80
62 agg gag cgc gag cgg cag ctg gcc aag cgc cag cac ctg gag gag cag      403
63 Arg Glu Arg Glu Arg Gln Leu Ala Lys Arg Gln His Leu Glu Glu Gln
64             85             90             95
68 cgg ctg cag cag gag cgg cag cgg gag cag cag cgg cgc gag cgc      451
69 Arg Leu Gln Glu Arg Gln Arg Glu Gln Glu Gln Arg Arg Glu Arg
70             100             105             110
72 aag cgt aag atc tcc tgc ctg tcc ttt gca cta gac gac ctc gat gac      499

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73 Lys Arg Lys Ile Ser Cys Leu Ser Phe Ala Leu Asp Asp Leu Asp Asp
74      115                      120                      125
76 cag gcc gac gcg gcc gag gcc agg cgc gcc gga aac ctg ggc aag aac      547
77 Gln Ala Asp Ala Ala Glu Ala Arg Arg Ala Gly Asn Leu Gly Lys Asn
78 130                      135                      140                      145
80 ccc gac gtg gac acc agc ttc ctg cca gac cgc gac cgc gag gag gag      595
81 Pro Asp Val Asp Thr Ser Phe Leu Pro Asp Arg Asp Arg Glu Glu Glu
82                      150                      155                      160
84 gag aac cgg ctc cga gag gag ctg cgc caa gag tgg gag gcg cag cgc      643
85 Glu Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Gln Arg
86                      165                      170                      175
88 gag aaa gtg aag gac gag gag atg gag gtc acc ttc agc tac tgg gac      691
89 Glu Lys Val Lys Asp Glu Glu Met Glu Val Thr Phe Ser Tyr Trp Asp
90      180                      185                      190
92 ggc tcg ggc cac cgg cgc acg gtg cgg gtg cgc aag ggc aac acg gtg      739
93 Gly Ser Gly His Arg Arg Thr Val Arg Val Arg Lys Gly Asn Thr Val
94      195                      200                      205
96 cag cag ttc ctg aag aag gcg ctg cag ggg ctg cgc aag gac ttc ctg      787
97 Gln Gln Phe Leu Lys Lys Ala Leu Gln Gly Leu Arg Lys Asp Phe Leu
98 210                      215                      220                      225
100 gag ctg cgc tcc gcc ggc gtg gag cag ctc atg ttc atc aag gag gac      835
101 Glu Leu Arg Ser Ala Gly Val Glu Gln Leu Met Phe Ile Lys Glu Asp
102                      230                      235                      240
104 ctc atc ctg ccg cac tac cac acc ttc tac gac ttc atc atc gcc agg      883
105 Leu Ile Leu Pro His Tyr His Thr Phe Tyr Asp Phe Ile Ile Ala Arg
106                      245                      250                      255
108 gcg agg ggc aag agc ggg ccg ctc ttc agc ttc gat gtg cac gat gac      931
109 Ala Arg Gly Lys Ser Gly Pro Leu Phe Ser Phe Asp Val His Asp Asp
110                      260                      265                      270
112 gtg cgc ctg ctc agc gac gcc acc atg gag aag gac gag tcg cac gcg      979
113 Val Arg Leu Leu Ser Asp Ala Thr Met Glu Lys Asp Glu Ser His Ala
114      275                      280                      285
116 ggc aag gtg gtg ctg cgc agc tgg tac gag aag aac aag cac atc ttc      1027
117 Gly Lys Val Val Leu Arg Ser Trp Tyr Glu Lys Asn Lys His Ile Phe
118 290                      295                      300                      305
120 ccc gcc agc cgc tgg gag gcc tat gac ccc gag aag aag tgg gac aag      1075
121 Pro Ala Ser Arg Trp Glu Ala Tyr Asp Pro Glu Lys Lys Trp Asp Lys
122                      310                      315                      320
124 tac acc atc cgc taacacccgc ctgccagagc ggaaaccggg ggtgggggga      1127
125 Tyr Thr Ile Arg
126      325
128 gacactcatt tctaggcccc atcaccagtc acttgatttc gtgacctga tttcttcccc      1187
130 caaattttaat aaagacagag ggttctcatg attcacattg gttgtgctat tgctgatgtt      1247
132 atgctttggt tgcttggttg gtcttttctg agtatttttag tgttgccacc tggatttgct      1307
134 gcattgctct gctgagctgt attgaaacca tgactgggcc cactgtcaga cagaaattag      1367
136 aataggaggc acatttttta cctgggtggt atgagcatgg acttgggggc cacagtgact      1427
138 gagtttgatt cccgacacag cctcctcctt gctgtgtagt tttgggtaag cttattaaac      1487
140 ccccatgcct cagtttggtc acctgtaaaa ggaaataaca agagcactta ctttataaga      1547
142 ttgatgtgag tattaagtga attaatatat gtaaaacgct tagctcttaa taaatgtttc      1607

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1618

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144 tgttggttatt a
148 <210> SEQ ID NO: 2
149 <211> LENGTH: 325
150 <212> TYPE: PRT
151 <213> ORGANISM: Human
153 <400> SEQUENCE: 2
156 Met Ala Gln Tyr Lys Gly Thr Met Arg Glu Ala Gly Arg Ala Met His
157   1           5           10           15
159 Leu Leu Lys Lys Arg Glu Arg Gln Arg Glu Gln Met Glu Val Leu Lys
160           20           25           30
162 Gln Arg Ile Ala Glu Glu Thr Ile Leu Lys Ser Gln Val Asp Lys Arg
163           35           40           45
165 Phe Ser Ala His Tyr Asp Ala Val Glu Ala Glu Leu Lys Ser Ser Thr
166           50           55           60
168 Val Gly Leu Val Thr Leu Asn Asp Met Lys Ala Arg Gln Glu Ala Leu
169   65           70           75           80
171 Val Arg Glu Arg Glu Arg Gln Leu Ala Lys Arg Gln His Leu Glu Glu
172           85           90           95
174 Gln Arg Leu Gln Gln Glu Arg Gln Arg Glu Gln Glu Gln Arg Arg Glu
175           100          105          110
177 Arg Lys Arg Lys Ile Ser Cys Leu Ser Phe Ala Leu Asp Asp Leu Asp
178           115          120          125
180 Asp Gln Ala Asp Ala Ala Glu Ala Arg Arg Ala Gly Asn Leu Gly Lys
181           130          135          140
183 Asn Pro Asp Val Asp Thr Ser Phe Leu Pro Asp Arg Asp Arg Glu Glu
184 145           150          155          160
186 Glu Glu Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Gln
187           165          170          175
189 Arg Glu Lys Val Lys Asp Glu Glu Met Glu Val Thr Phe Ser Tyr Trp
190           180          185          190
192 Asp Gly Ser Gly His Arg Arg Thr Val Arg Val Arg Lys Gly Asn Thr
193           195          200          205
195 Val Gln Gln Phe Leu Lys Lys Ala Leu Gln Gly Leu Arg Lys Asp Phe
196           210          215          220
198 Leu Glu Leu Arg Ser Ala Gly Val Glu Gln Leu Met Phe Ile Lys Glu
199 225           230          235          240
201 Asp Leu Ile Leu Pro His Tyr His Thr Phe Tyr Asp Phe Ile Ile Ala
202           245          250          255
204 Arg Ala Arg Gly Lys Ser Gly Pro Leu Phe Ser Phe Asp Val His Asp
205           260          265          270
207 Asp Val Arg Leu Leu Ser Asp Ala Thr Met Glu Lys Asp Glu Ser His
208           275          280          285
210 Ala Gly Lys Val Val Leu Arg Ser Trp Tyr Glu Lys Asn Lys His Ile
211           290          295          300
213 Phe Pro Ala Ser Arg Trp Glu Ala Tyr Asp Pro Glu Lys Lys Trp Asp
214 305           310          315          320
216 Lys Tyr Thr Ile Arg
217           325
220 <210> SEQ ID NO: 3

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221 <211> LENGTH: 2875
222 <212> TYPE: DNA
223 <213> ORGANISM: Human
225 <400> SEQUENCE: 3
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230 gcatgttaga ggctcacagt aaagacactg ctacacttta actcagtgtc ccatggttat      120
232 tagagcttag aaccggggg aaactgctgt atagaagagg tcaaacaagc tgagtgcagg      180
234 ttttgtcacg aaactggggg gcgagtaggg ttctattatc aaagaatggg tgtgttgggg      240
236 ccataagaaa gaattacagg cagtgtgtgc caggtaatgt tcacgagacg ccacagcggg      300
238 gtagcatcag aggcgggagg aggagggttg gagagcaggg cgtgtttgca aggtctctctg      360
240 ggtggccaca gcagcttgcg ctgcgcccac attgcttctg cgtgtttaca gctgggcacg      420
242 agaaggtca gcacgcacgc acagcaggty ggggcccgcc ctgccacag cgtgaaaaca      480
244 ggagccccgg ccagccacgg ctgggcaggg ccagaagcgc ctctccagg atcctccccg      540
246 cgctggcccc cccacagga gcaccgcccc taccaggagc ccggagctct tcccagggcc      600
248 cgctccccgg ccagggggcg atccacctcc acttctgtgt tccgcagccg ccctaccagg      660
250 agcctggcac tctctcagg gccgcctcc ccgccagggg gcgcaccgcc tccacttctc      720
252 gtgtccacgg ctgtcgcgag agcccggggc gagtgggect ctgctcgtgg gtggttctcg      780
254 tggaggtcag ctcccgctg tctccgctcg acagggtgct tgggcaggta agggctccgt      840
256 cagtagccca accctctctg tatgcagctc cccaaattca gcgctgcgct caggcatggc      900
258 agccaccctg tacgtggggc cgttcgcatt tgcatttatt gaggtcaaataaaaatgctgg      960
260 aaattggtgc ctggtgacac tgtcaggttg gtggttaccc tagcaggtcg gccagcccc      1020
262 tgaacgcttc catcacctgc gaaagccctg tgaggaggcg cagagctgag cattccccgc      1080
264 cgctgcgtgg gccccctct acctgccgcg ttttctctct ttgctgcaga gcccatcggg      1140
266 taggcgcggg ccatggcgca gtacaagggc accatgcgcg aggcaggccg tgccatgcac      1200
268 ctctcaaga agcgcgaaag gcagcgggag cagatggagg tgctgaagca gcgcatcgcc      1260
270 gaggagacca tctcaagtc gcaggtggac aagaggttct cggcgcatca cgacgcctg      1320
272 gaggccgagc tgaagtccag cacggtgggc ctggtgacct tgaacgacat gaaggcccg      1380
274 caggaggccc tggtcaggga gcgcgagcgg cagctggcca agcgcagca cctggaggag      1440
276 cagcggctgc agcaggagcg gcagcgggag caggagcagc ggcgcgagcg caagcgtaag      1500
278 atctcttgc tgctcttgc actagacgac ctcatgacc aggcgcagcg ggccgaggcc      1560
280 aggcgcgccc gaaacctgg caagaacccc gacgtggaca ccagcttctt gccagaccgc      1620
282 gaccgcgagg aggaggagaa ccggctccga gaggagctgc gccaaagagt ggaggcgag      1680
284 cgcgagaaag tgaaggacga ggagatggag gtcaccttca gctactggga cggctcgggc      1740
286 caccggcgca cggtgcggt gcgcaagggc aacacggtgc agcagttcct gaagaaggcg      1800
288 ctgcaggggc tgcgcaagga ctctctggag ctgcgctccg ccggcggtga gcagctcatg      1860
290 ttcatcaagg aggacctcat cctgccgcac taccacacct tctacgactt catcatcgcc      1920
292 agggcgagg gcaagagcgg gccgctcttc agcttcgatg tgcacgatga cgtgcgectg      1980
294 ctacgcgacg ccaccatgga gaaggacgag tcgacgcgg gcaaggtggg gctgcgcagc      2040
296 tggtagcaga agaacaagca catcttcccc gccagccgct gggaggccta tgaccccgag      2100
298 aagaagtggg acaagtacac catccgctaa caccgcctg ccagagcgga aaccgggggt      2160
300 ggggggagac actcatttct agggcccatc accagtcact tgatttcgtg accttgattt      2220
302 ctcccccaa atttaataa gacagagggt tctcatgatt cacattgggt gtgctattgc      2280
304 tgatgttatg ctttggttgc ttggttggtc ttttctgagt attttagtgt tgccacctgg      2340
306 atttgctgca ttgctctgct gagctgtatt gaaacctatg ctgggcccac tgtcagacag      2400
308 aaattagaat aggaggcaca ttttttacct ggtggttatg agcatggact tgggggccac      2460
310 agtgactgag tttgattccc gacacagcct cctccttgct gtgtagtttt gggtaaagctt      2520
312 attaaacccc catgcctcag tttggtcacc tgtaaaggga aataacaaga gcacttactt      2580
314 tataagattg atgtgagtat taagtgaatt aatatttgta aaacgcttag ctcttaataa      2640
316 atgtttctgt tgttattatt atggttttgg ttaatttatt taaaggactg caatgaccta      2700

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318 gttcagaact atttgagggc aaaggtggac ctgcccatca ctggtcccag gatcagcagt      2760
320 tgccagcagg agggggctag caaaggttgg ggagcagccc ccctctagtg ggcttttagct      2820
322 gggttgttta gcccagaagt taggaggaca gtgagctaata gcaagtagcc tgcag          2875
326 <210> SEQ ID NO: 4
327 <211> LENGTH: 1217
328 <212> TYPE: DNA
329 <213> ORGANISM: Mouse
331 <220> FEATURE:
332 <221> NAME/KEY: cDS
333 <222> LOCATION: (137)..(1138)
335 <400> SEQUENCE: 4
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340 gaactgacat cagaccaga aggctaccag aaacagggac tgggcaggcc aaaaagcctt      120
342 gcgctgaact gcaggc atg gcg cag tac aaa ggc acc atg cgg gaa gct          169
343           Met Ala Gln Tyr Lys Gly Thr Met Arg Glu Ala
344           1             5             10
346 ggc cgg gcc atg cac ctg atc aag aag cgt gag aag cag aag gag cag      217
347 Gly Arg Ala Met His Leu Ile Lys Lys Arg Glu Lys Gln Lys Glu Gln
348           15             20             25
350 atg gag gtg ctg aag cag cgc atc gca gag gag acc atc atg aag tca      265
351 Met Glu Val Leu Lys Gln Arg Ile Ala Glu Glu Thr Ile Met Lys Ser
352           30             35             40
354 aaa gtg gac aag aag ttc tgc gca cac tac gac gcc gtg gag gcc gag      313
355 Lys Val Asp Lys Lys Phe Ser Ala His Tyr Asp Ala Val Glu Ala Glu
356           45             50             55
358 ctg aag tcc agt acg gtg ggc ctg gtg acc ctg aat gac atg aag gcc      361
359 Leu Lys Ser Ser Thr Val Gly Leu Val Thr Leu Asn Asp Met Lys Ala
360 60             65             70             75
362 aag cag gag gcc ctg ctg agg gag cgg gag atg cag ctg gcc aag agg      409
363 Lys Gln Glu Ala Leu Leu Arg Glu Arg Glu Met Gln Leu Ala Lys Arg
364           80             85             90
366 gag cag ctg gag caa cgc cgg ata cag ctg gag atg ctg cgc gag aag      457
367 Glu Gln Leu Glu Gln Arg Arg Ile Gln Leu Glu Met Leu Arg Glu Lys
368           95             100            105
370 gag cga agg cga gag cgc aag cgc aag atc tcc aac ctg tct ttc acg      505
371 Glu Arg Arg Arg Glu Arg Lys Arg Lys Ile Ser Asn Leu Ser Phe Thr
372           110            115            120
374 ttg gac gag gaa gaa ggt gac caa gag gac agc cgc caa gcc gag agt      553
375 Leu Asp Glu Glu Glu Gly Asp Gln Glu Asp Ser Arg Gln Ala Glu Ser
376           125            130            135
378 gcc gag gcc cac agt gct gga gcc aag aag aac ttg ggc aag aat ccc      601
379 Ala Glu Ala His Ser Ala Gly Ala Lys Lys Asn Leu Gly Lys Asn Pro
380 140            145            150            155
382 gat gtg gac acg agc ttc ctg ccc gac cgc gag cgc gag gag gag gag      649
383 Asp Val Asp Thr Ser Phe Leu Pro Asp Arg Glu Arg Glu Glu Glu Glu
384           160            165            170
386 aac cgg ttg cgc gag gaa ctg cgg cag gag tgg gag gcg aag cgc gag      697
387 Asn Arg Leu Arg Glu Glu Leu Arg Gln Glu Trp Glu Ala Lys Arg Glu
388           175            180            185

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date